

Database : GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vi:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htg_mus:*
- 34: em_htg_pln:*
- 35: em_htg_rod:*
- 36: em_htg_mam:*
- 37: em_htg_vrt:*
- 38: em_sy:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	2925	100.0	2925	6	BD265755	BD265755 New metal
2	2925	100.0	2925	6	AX033272	AX033272 Sequence
3	2925	100.0	2925	10	AF176569	AF176569 Mus muscu
4	2852	97.5	2892	6	AR306357	AR306357 Sequence
5	2852	97.5	2892	6	BD062349	BD062349 Membrane-

relevant
2000
2003
2002

6	2852	97.5	2892	10	AF157105
7	2704	92.4	2823	6	AR306358
8	2704	92.4	2823	6	BD062350
9	2610	89.2	2652	10	AF302076
10	2483.6	84.9	2601	10	AF157106
11	2462	84.2	2583	10	AF302075
12	2341	80.0	2694	10	AF302077
13	2284.2	78.1	2765	6	AX014701
14	2284.2	78.1	2765	6	BD204629
15	1612.8	55.1	2850	6	AX747891
16	1612.8	55.1	2850	9	AK093058
17	1612.8	55.1	2893	6	AX356951
18	1612.8	55.1	2893	6	AX463057
19	1612.8	55.1	2893	6	AX665155
20	1612.8	55.1	2893	6	AX794730
21	1612.8	55.1	2975	6	AX356955
22	1612.8	55.1	2975	6	AX463058
23	1612.8	55.1	2975	6	AX665159
24	1612.8	55.1	2975	6	AX794731
25	1611.2	55.1	2953	6	AX473100
26	1607.4	55.0	2714		

11/1999

AF157105	Mus muscu
AR306358	Sequence
BD062350	Membrane-
AF302076	Mus muscu
AF157106	Mus muscu
AF302075	Mus muscu
AF302077	Mus muscu
AX014701	Sequence
BD204629	Novel mem
AX747891	Sequence
AK093058	Homo sapi
AX356951	Sequence
AX463057	Sequence
AX665155	Sequence
AX794730	Sequence
AX356955	Sequence
AX463058	Sequence
AX665159	Sequence
AX794731	Sequence
AX473100	Sequence

Database : N_Geneseq_29Jan04:*
 1: geneseqn1980s:*
 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002s:*
 7: geneseqn2003as:*
 8: geneseqn2003bs:*
 9: geneseqn2003cs:*
 10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query		DB		ID	Description
No.	Score	Match	Length				
1	2925	100.0	2925	3	AAA63763	app	Aaa63763 cDNA enco
2	2284.2	78.1	2765	2	AAZ28810		Aaz28810 Rat membr
3	1840.6	62.9	2286	6	AAD28130		Aad28130 Soluble s
4	1612.8	55.1	2850	9	ADB63262		Adb63262 Human cDN
5	1612.8	55.1	2893	6	AAD28544		Aad28544 Human sol
6	1612.8	55.1	2893	6	ABN84279		Abn84279 Human SEP
7	1612.8	55.1	2893	8	ADB61387		Adb61387 cDNA of h
8	1612.8	55.1	2975	6	AAD28547		Aad28547 Human SEP
9	1612.8	55.1	2975	8	ADB61388		Adb61388 Human sol
10	1611.2	55.1	2953	6	ABK48251		Abk48251 cDNA enco
11	1607.4	55.0	2714	4	AAF59659		Aaf59659 Human nep

Database : EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					Description
	No.	Score	Match	Length	DB ID	
	1	662.2	22.6	2253	29	AY413138
	2	662.2	22.6	3693	11	AK033824
	3	662.2	22.6	4241	11	AK031446
	4	652	22.3	678	13	BY747982
	5	649.4	22.2	2253	29	AY413136
	6	645	22.1	2253	29	AY413137
c	7	642	21.9	704	12	BG153322
	8	640.8	21.9	3320	11	AK076908
	9	587.6	20.1	595	14	CF106429
	10	542	18.5	600	12	BI989738
	11	525.2	18.0	625	13	BY727098
	12	425.2	14.5	439	13	BY463004
	13	396.4	13.6	402	13	BY533520
	14	395.8	13.5	424	13	BY454450
c	15	391.4	13.4	507	10	BE106100
	16	382.2	13.1	419	13	BY446300
	17	381.8	13.1	400	13	BY533195

18	380.2	13.0	395	13	BY523048
19	378	12.9	378	9	AA146423
20	376	12.9	401	13	

BY523048 BY523048
AA146423 mr66e08.r

Database : A_Geneseq_29Jan04:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Match	Length			
1	4042	100.0	765	3	AAB08130	Aab08130 A murine
2	3677	91.0	774	2	AAY44177	Aay44177 Rat membr
3	3523	87.2	746	5	AAE17781	Aae17781 Soluble s
4	3252.5	80.5	770	3	AAB08131	Aab08131 A human n
5	3252.5	80.5	779	5	AAE17779	Aae17779 Human sol
6	3252.5	80.5	779	5	ABB79521	Abb79521 Human SEP
7	3252.5	80.5	779	5	AAU78850	Aau78850 Novel nep
8	3252.5	80.5	779	7	ADB61389	Adb61389 Human sol
9	3251.5	80.4	779	4	AAB83841	Aab83841 Amino aci
10	3251.5	80.4	779	6	AAE33307	Aae33307 Human met
11	3250.5	80.4	779	7	ADB65232	Adb65232 Human pro
12	3249.5	80.4	779	4	AAB60561	Aab60561 Human nep
13	3195.5	79.1	753	4	AAB83842	Aab83842 Amino aci
14	3195.5	79.1	753	6	AAE33308	Aae33308 Human met
15	3193.5	79.0	753	4	AAB60562	Aab60562 Human nep
16	3156.5	78.1	742	5	AAE19176	Aae19176 Human pro

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	4042	100.0	765	12	US-10-267-502-257	Sequence 257, App
2	3252.5	80.5	770	12	US-10-267-502-251	Sequence 251, App
3	3252.5	80.5	779	9	US-09-905-846-2	Sequence 2, Appli
4	3252.5	80.5	779	12	US-10-423-543-58	Sequence 58, Appl
5	3252.5	80.5	779	12	US-09-928-531-2	Sequence 2, Appli
6	3252.5	80.5	779	14	US-10-017-273A-6	Sequence 6, Appli
7	3252.5	80.5	779	15	US-10-192-407C-2	Sequence 2, Appli
8	3251.5	80.4	779	14	US-10-147-928-4	Sequence 4, Appli
9	3251.5	80.4	779	16	US-10-715-112-4	Sequence 4, Appli
10	3250.5	80.4	779	15	US-10-104-047-3386	Sequence 3386, Ap
11	3195.5	79.1	753	14	US-10-147-928-6	Sequence 6, Appli
12	3195.5	79.1	753	16	US-10-715-112-6	Sequence 6, Appli
13	3156.5	78.1	742	15	US-10-274-639-13	Sequence 13, Appl
14	3156.5	78.1	742	16	US-10-333-574-13	Sequence 13, Appl

Database : PIR_78:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3677	91.0	774	2	JC7265	neprilysin (EC 3.4
2	2124	52.5	750	1	HYHUN	neprilysin (EC 3.4
3	2124	52.5	750	1	HYRTN	neprilysin (EC 3.4
4	2108.5	52.2	751	1	HYRBN	neprilysin (EC 3.4
5	1491	36.9	754	2	A53679	endothelin convert
6	1490	36.9	758	2	JC2521	endothelin convert
7	1490	36.9	770	2	JC4136	endothelin convert
8	1485	36.7	758	2	A54667	endothelin convert
9	1483	36.7	754	2	S47268	endothelin-convert
10	1381.5	34.2	825	2	I46078	endothelin convert
11	1335.5	33.0	750	2	D88082	protein T05A8.4 [i
12	1140.5	28.2	766	2	T20003	hypothetical prote
13	1090.5	27.0	590	2	C88099	protein F18A12.8 [
14	1056	26.1	769	2	T24949	hypothetical prote
15	943.5	23.3	754	2	T16182	hypothetical prote
16	807.5	20.0	706	2	F87683	peptidase M13 fami
17	803	19.9	700	2	B82788	metallopeptidase X

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2131	52.7	749	1	NEP_MOUSE	Q61391 mus musculu
2	2124	52.5	749	1	NEP_HUMAN	P08473 homo sapien
3	2124	52.5	749	1	NEP_RAT	P07861 rattus norv
4	2119	52.4	749	1	NEP_RABIT	P08049 oryctolagus
5	1491.5	36.9	762	1	ECE1_RAT	P42893 rattus norv
6	1490	36.9	770	1	ECE1_HUMAN	P42892 homo sapien
7	1487	36.8	754	1	ECE1_CAVPO	P97739 cavia porce
8	1483	36.7	754	1	ECE1_BOVIN	P42891 bos taurus
9	1430.5	35.4	787	1	ECE2_HUMAN	O60344 homo sapien
10	1381.5	34.2	787	1	ECE2_BOVIN	Q10711 bos taurus
11	1378.5	34.1	749	1	PEX_MOUSE	P70669 mus musculu
12	1377.5	34.1	749	1	PEX_HUMAN	P78562 homo sapien
13	1262	31.2	775	1	ECEL_HUMAN	O95672 homo sapien
14	1253.5	31.0	775	1	ECEL_MOUSE	Q9jmi0 mus musculu

Database : SPTREMBL_25:*
 1: sp_archaea:*
 2: sp_bacteria:*
 3: sp_fungi:*
 4: sp_human:*
 5: sp_invertebrate:*
 6: sp_mammal:*
 7: sp_mhc:*
 8: sp_organelle:*
 9: sp_phage:*
 10: sp_plant:*
 11: sp_rodent:*
 12: sp_virus:*
 13: sp Vertebrate:*
 14: sp_unclassified:*
 15: sp_rvirus:*
 16: sp_bacteriap:*
 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Pred. No.	Description
1	4042	100.0	765	11	Q9JLI3	2000	Q9jli3 mus musculu
2	4028	99.7	765	11	Q9QZV7	11/1999	Q9qzv7 mus musculu
3	3900.5	96.5	742	11	Q9ERK3	2001	Q9erk3 mus musculu
4	3886.5	96.2	742	11	Q9QZV6	11/1999	Q9qzv6 mus musculu
5	3872	95.8	779	11	Q9ERK2	2001	Q9erk2 mus musculu
6	3252.5	80.5	770	4	Q96PH9		Q96ph9 homo sapien
7	2140	52.9	750	11	Q8K251		Q8k251 mus musculu
8	1925.5	47.6	770	13	O93394		O93394 perca flave
9	1514	37.5	849	5	Q9W436		Q9w436 drosophila
10	1490	36.9	758	6	Q28868		Q28868 bos taurus
11	1485	36.7	758	6	Q28010		Q28010 bos taurus
12	1481	36.6	727	5	Q8IS64		Q8is64 locusta mig
13	1460.5	36.1	752	13	Q7ZTK3		Q7ztk3 xenopus lae
14	1455	36.0	752	13	Q9DGN6		Q9dgn6 gallus gall
15	1431	35.4	811	4	Q8NFD7		Q8nfd7 homo sapien
16	1413.5	35.0	763	11	Q923T6		Q923t6 mus musculu
17	1411.5	34.9	976	5	Q9I7I4		Q9i7i4 drosophila
18	1411.5	34.9	1040	5	Q8T062		Q8t062 drosophila

RESULT 1

Q9JLI3

ID Q9JLI3 PRELIMINARY; PRT; 765 AA.
AC Q9JLI3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Neprilysin-like metallopeptidase 1 (Neprilysin-like peptidase
DE beta).
GN MELL1 OR SEP OR NL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX PubMed=10749671;
RA Ghaddar G., Ruchon A.F., Carpentier M., Marcinkiewicz M., Seidah N.G.,
RA Crine P., DesGroseillers L., Boileau G.;
RT "Molecular cloning and biochemical characterization of a new mouse
RT testis soluble zinc-metallopeptidase of the neprilysin family.";
RL Biochem. J. 347:419-429(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Shirotani K., Saïdo T.C.;
RT "Cloning of neprilysin-like peptidase cDNAs.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF176569; AAF69247.1; -.
DR EMBL; AF302076; AAG18447.1; -.
DR HSSP; P08473; 1DMT.
DR MEROPS; M13.008; -.
DR MGD; MGI:1351603; Mell1.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0005794; C:Golgi apparatus; IDA.
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR008753; Peptidase_M13_N.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01431; Peptidase_M13; 1.
DR Pfam; PF05649; Peptidase_M13_N; 1.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 765 AA; 88699 MW; D3662F1CE5B957F7 CRC64;

Query Match 100.0%; Score 4042; DB 11; Length 765;
Best Local Similarity 100.0%; Pred. No. 2.5e-237;
Matches 765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 MVERAGWCRKKS PGFVEYGLMVLLLLLLGAIIVTLG VFYSIGKQLPLLTSL LHFSWDERTV 60
      |||
Db      1 MVERAGWCRKKS PGFVEYGLMVLLLLLLGAIIVTLG VFYSIGKQLPLLTSL LHFSWDERTV 60

QY      61 VKRALRDSSLKSDICTTPSCVIAAARILENMDQSRNPCENFYQYACGGWLRHHVIPETNS 120
      |||
Db      61 VKRALRDSSLKSDICTTPSCVIAAARILENMDQSRNPCENFYQYACGGWLRHHVIPETNS 120

QY      121 RYSVFDILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLK 180
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Db      121 RYSVFDILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLK 180
Qy      181 MVGGWPVAMDKWNETMGLKWELERQLAVLNSQFNRRVLIDLFIWNDDQNSSRHVIYIDQP 240
Db      181 MVGGWPVAMDKWNETMGLKWELERQLAVLNSQFNRRVLIDLFIWNDDQNSSRHVIYIDQP 240
Qy      241 TLGMPsREYYFQEDNNHKVRKAYLEFMTSVATMLRKDQNLskESAMVREEMAeVLELETH 300
Db      241 TLGMPsREYYFQEDNNHKVRKAYLEFMTSVATMLRKDQNLskESAMVREEMAeVLELETH 300
Qy      301 LANATVPQEKRHdVTALYHRMDLMELQERFGLKGFNWTLFIQNLSSVEVELFPDEEVVV 360
Db      301 LANATVPQEKRHdVTALYHRMDLMELQERFGLKGFNWTLFIQNLSSVEVELFPDEEVVV 360
Qy      361 YGIPYLENLEDIIDSYSARTMQNYLVWRLVLDRIgSLsQRfKEARVDYRKALYgTTVEEV 420
Db      361 YGIPYLENLEDIIDSYSARTMQNYLVWRLVLDRIgSLsQRfKEARVDYRKALYgTTVEEV 420
Qy      421 RWRECVSYVNSNMESAVGSLYIKRAFskDSKSTVRELIEKIRSVFVDNLDELNWMDEESK 480
Db      421 RWRECVSYVNSNMESAVGSLYIKRAFskDSKSTVRELIEKIRSVFVDNLDELNWMDEESK 480
Qy      481 KKAQEKAMNIREQIGYPDYILEDNNKHLDEEYSSLTfYEDLYFENGLQNLKNNaQRSLKK 540
Db      481 KKAQEKAMNIREQIGYPDYILEDNNKHLDEEYSSLTfYEDLYFENGLQNLKNNaQRSLKK 540
Qy      541 LREKVDQNLWIIGAaVNAFYSpNRnQIVFPAGILQPPFFSKDQPQSLNFGGIGMvIGHE 600
Db      541 LREKVDQNLWIIGAaVNAFYSpNRnQIVFPAGILQPPFFSKDQPQSLNFGGIGMvIGHE 600
Qy      601 ITHGFDDNGRNFDKNGNMLDwWSNFSARHFQQSQCMiYQYGNFSWELADNQNvNGFSTL 660
Db      601 ITHGFDDNGRNFDKNGNMLDwWSNFSARHFQQSQCMiYQYGNFSWELADNQNvNGFSTL 660
Qy      661 GENIADNGGVRQAYKAYLRWLADGGKDQRLPGLNLTYAQLFFINyaQVWCGSYRPEFAVQ 720
Db      661 GENIADNGGVRQAYKAYLRWLADGGKDQRLPGLNLTYAQLFFINyaQVWCGSYRPEFAVQ 720
Qy      721 SIKTDVHSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPMKRCRIW 765
Db      721 SIKTDVHSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPMKRCRIW 765

```

RESULT 2

Q9QZV7

```

ID   Q9QZV7          PRELIMINARY;          PRT;    765 AA.
AC   Q9QZV7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Soluble secreted endopeptidase.
GN   MELL1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;

```

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20011457; PubMed=10542292;
 RA Ikeda K., Emoto N., Raharjo S.B., Nurhantari Y., Saiki K.,
 RA Yokoyama M., Matsuo M.;
 RT "Molecular identification and characterization of novel membrane-bound
 RT metalloprotease, the soluble secreted form of which hydrolyzes a
 RT variety of vasoactive peptides.";
 RL J. Biol. Chem. 274:32469-32477(1999).
 DR EMBL; AF157105; AAF13152.1; -.
 DR HSSP; P08473; 1DMT.
 DR MEROPS; M13.008; -.
 DR MGD; MGI:1351603; Mell1.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0005794; C:Golgi apparatus; IDA.
 DR InterPro; IPR000718; Peptidase_M13.
 DR InterPro; IPR008753; Peptidase_M13_N.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR Pfam; PF01431; Peptidase_M13; 1.
 DR Pfam; PF05649; Peptidase_M13_N; 1.
 DR PRINTS; PR00786; NEPRILYSIN.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 SQ SEQUENCE 765 AA; 88651 MW; 567D3C17764C0F3F CRC64;

→ November 5, 1999

Query Match 99.7%; Score 4028; DB 11; Length 765;
 Best Local Similarity 99.6%; Pred. No. 1.8e-236;
 Matches 762; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY	1	MVERAGWCRKKSPGFVEYGLMVL	60
Db	1	MVERAGWCRKKSPGFVEYGLMVL	60
QY	61	VKRALRDSSLKSDICTTPSCVIAAARILENMDQSRNPCENFYQYACGGWLRHHVIPETNS	120
Db	61	VKRALRDSSLKSDICTTPSCVIAAARILENMDQSRNPCENFYQYACGGWLRHHVIPETNS	120
QY	121	RYSVFDILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLK	180
Db	121	RYSVFDILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLK	180
QY	181	MVGGWPVAMDKWNETMGLKWELERQLAVLNSQFNRRVLIDLFIWNDDQSSRHVIYIDQP	240
Db	181	MVGGWPVALDKWNETMGLKWELERQLAVLNSQFNRRVLIDLFIWNDDQSSRHVIYIDQP	240
QY	241	TLGMPREYYFQEDNNHKVRKAYLEFMTSVATMLRKDQNLKESAMVREEMAEVLELETH	300
Db	241	TLGMPREYYFQEDNNHKVRKAYLEFMTSVATMLRKDQNLKESAMVREEMAEVLELETH	300
QY	301	LANATVPQEKRDVTALYHRMDLMELQERFGLKGFNWTLFIQNVLSSVEVELFPDEEVVV	360
Db	301	LANATVPQEKRDVTALYHRMDLMELQERFGLKGFNWTLFIQNVLSSVEVELFPDEEVVV	360
QY	361	YGIPYLENLEDIIDSYSARTMQNYLVWRLVLDRIKSLQRFKEARVDYRKALYGTTEEV	420
Db	361	YGIPYLENLEDIIDSYSARTMQNYLVWRLVLDRIKSLQRFKEARVDYRKALYGTTEEV	420
QY	421	RWRECVSYVNSNMESAVGSLYIKRAFSDKSKSTVRELIEKIRSVFDNLDLNMDEESK	480

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Db      421  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 480
      481  KKAQEKAMNIREQIGYPDYILEDNNKHLDEEYSSLTFYEDLYFENGLQNLKNNQQRSLKK 540
      481  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 540
      481  KKAQEKAMNIREQIGYPDYILEDNNKHLDEEYSSLTFYEDLYFENGLQNLKNNQQRSLKK 540
Qy      541  LREKVDQNLWIIGAAVVNAFYSPNRNQIVFPAGILQPPFFSKDQPQSLNFGGIGMVGHE 600
      541  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 600
Db      541  LREKVDQNLWIIGAAVVNAFYSPNRNQIVFPAGILQPPFFSKDQPQSLNFGGIGMVGHE 600
Qy      601  ITHGFDDNGRNFDKNGNMLDWWSNFSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSTL 660
      601  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:| 660
Db      601  ITHGFDDNGRNFDKNGNMLDWWSNFSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSSL 660
Qy      661  GENIADNGGVRQAYKAYLRWLADGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQ 720
      661  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 720
Db      661  GENIADNGGVRQAYKAYLRWLADGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQ 720
Qy      721  SIKTDVHSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPMKRCRIW 765
      721  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 765
Db      721  SIKTDVHSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPMKRCRIW 765

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RESULT 3

Q9ERK3

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ID   Q9ERK3      PRELIMINARY;      PRT;      742 AA.
AC   Q9ERK3;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Neprilysin-like peptidase alpha.
GN   MELL1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21293028; PubMed=11278416;
RA   Shirotani K., Tsubuki S., Iwata N., Takaki Y., Harigaya W.,
RA   Maruyama K., Kiryu-Seo S., Kiyama H., Iwata H., Tomita T.,
RA   Iwatsubo T., Saido T.C.;
RT   "Neprilysin Degrades Both Amyloid beta Peptides 1-40 and 1-42 Most
RT   Rapidly and Efficiently among Thiorphan- and Phosphoramidon-sensitive
RT   Endopeptidases.";
RL   J. Biol. Chem. 276:21895-21901(2001).
DR   EMBL; AF302075; AAG18446.1; -.
DR   HSSP; P08473; 1DMT.
DR   MEROPS; M13.008; -.
DR   MGD; MGI:1351603; Mell1.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0005794; C:Golgi apparatus; IDA.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR008753; Peptidase_M13_N.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   Pfam; PF01431; Peptidase_M13; 1.

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DR Pfam; PF05649; Peptidase_M13_N; 1.
 DR PRINTS; PR00786; NEPRILYSIN.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 SQ SEQUENCE 742 AA; 85993 MW; 4A44EAD211B2499F CRC64;

Query Match 96.5%; Score 3900.5; DB 11; Length 742;
 Best Local Similarity 97.0%; Pred. No. 9.5e-229;
 Matches 742; Conservative 0; Mismatches 0; Indels 23; Gaps 1;

Qy	1	MVERAGWCRKKS	PGFVEYGLMVL	LLLLLL	LGAI	VT	LG	VF	YS	IG	KQLP	LL	TS	LL	HF	SW	DERT	V	60
Db	1	MVERAGWCRKKS	PGFVEYGLMVL	LLLLLL	LGAI	VT	LG	VF	YSI										40
Qy	61	VKRALR	DSSLKSDI	CTTP	SCVIAA	ARILE	NMDQ	SRNP	CENFY	QYAC	GGWLR	RHHV	IPETNS						120
Db	41	---	ALR	DSSLKSDI	CTTP	SCVIAA	ARILE	NMDQ	SRNP	CENFY	QYAC	GGWLR	RHHV	IPETNS					97
Qy	121	RYSV	FDILR	DELEV	ILKGV	LED	STS	QHR	PAVE	KAK	TLYR	SCMN	QSVIE	KRD	SE	PL	LSV	LK	180
Db	98	RYSV	FDILR	DELEV	ILKGV	LED	STS	QHR	PAVE	KAK	TLYR	SCMN	QSVIE	KRD	SE	PL	LSV	LK	157
Qy	181	MVGG	WPVAM	DKW	NETM	GLK	WELER	QLAV	LSQF	NRRV	LIDL	FI	WN	DD	QN	SS	RHV	IY	IDQP
Db	158	MVGG	WPVAM	DKW	NETM	GLK	WELER	QLAV	LSQF	NRRV	LIDL	FI	WN	DD	QN	SS	RHV	IY	IDQP
Qy	241	TLG	MP	SRE	YFQ	ED	NNH	KVR	KAY	LE	FMT	SV	AT	ML	RK	DQ	NLS	KES	AM
Db	218	TLG	MP	SRE	YFQ	ED	NNH	KVR	KAY	LE	FMT	SV	AT	ML	RK	DQ	NLS	KES	AM
Qy	301	LAN	AT	V	P	Q	E	K	R	H	D	V	T	A	L	Y	H	R	M
Db	278	LAN	AT	V	P	Q	E	K	R	H	D	V	T	A	L	Y	H	R	M
Qy	361	YGI	P	Y	L	E	N	L	E	D	I	I	D	S	A	R	T	M	Q
Db	338	YGI	P	Y	L	E	N	L	E	D	I	I	D	S	A	R	T	M	Q
Qy	421	RW	R	E	C	V	S	Y	V	N	S	N	M	E	S	A	V	G	S
Db	398	RW	R	E	C	V	S	Y	V	N	S	N	M	E	S	A	V	G	S
Qy	481	KKA	Q	E	K	A	M	N	I	R	E	Q	I	G	Y	P	D	Y	I
Db	458	KKA	Q	E	K	A	M	N	I	R	E	Q	I	G	Y	P	D	Y	I
Qy	541	LRE	K	V	D	Q	N	L	W	I	I	G	A	A	V	N	A	F	S
Db	518	LRE	K	V	D	Q	N	L	W	I	I	G	A	A	V	N	A	F	S
Qy	601	I	T	H	G	F	D	D	N	G	R	N	F	D	K	N	G	N	M
Db	578	I	T	H	G	F	D	D	N	G	R	N	F	D	K	N	G	N	M
Qy	661	GEN	I	A	D	N	G	G	V	R	Q	A	Y	K	A	Y	L	R	W
Db	638	GEN	I	A	D	N	G	G	V	R	Q	A	Y	K	A	Y	L	R	W

QY 721 SIKTDVHSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPMKRCRIW 765
 |||
 Db 698 SIKTDVHSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPMKRCRIW 742

RESULT 4
 Q9QZV6

ID Q9QZV6 PRELIMINARY; PRT; 742 AA.
 AC Q9QZV6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Soluble secreted endopeptidase delta.
 GN MELL1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20011457; PubMed=10542292;
 RA Ikeda K., Emoto N., Raharjo S.B., Nurhantari Y., Saiki K.,
 RA Yokoyama M., Matsuo M.;
 RT "Molecular identification and characterization of novel membrane-bound
 RT metalloprotease, the soluble secreted form of which hydrolyzes a
 RT variety of vasoactive peptides."
 RL J. Biol. Chem. 274:32469-32477(1999).
 DR EMBL; AF157106; AAF13153.1; -.
 DR HSSP; P08473; 1DMT.
 DR MEROPS; M13.008; -.
 DR MGD; MGI:1351603; Mell1.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0005794; C:Golgi apparatus; IDA.
 DR InterPro; IPR000718; Peptidase_M13.
 DR InterPro; IPR008753; Peptidase_M13_N.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR Pfam; PF01431; Peptidase_M13; 1.
 DR Pfam; PF05649; Peptidase_M13_N; 1.
 DR PRINTS; PR00786; NEPRILYSIN.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 SQ SEQUENCE 742 AA; 85945 MW; CF5FF9D982471157 CRC64;

Query Match 96.2%; Score 3886.5; DB 11; Length 742;
 Best Local Similarity 96.6%; Pred. No. 6.7e-228;
 Matches 739; Conservative 2; Mismatches 1; Indels 23; Gaps 1;

QY 1 MVERAGWCRKKS PGFVEYGLMVLLLLLLLGAI VTLGVFY SIGKQLPLLTSL LHF SWDERTV 60
 |||
 Db 1 MVERAGWCRKKS PGFVEYGLMVLLLLLLLGAI VTLGVFY SI----- 40
 QY 61 VKRALRDSS LKSDICTTPSCVIAAARILENMDQSRNPCENFYQYACGGWLRHHVIPETNS 120
 |||
 Db 41 ---ALRDSS LKSDICTTPSCVIAAARILENMDQSRNPCENFYQYACGGWLRHHVIPETNS 97
 QY 121 RYSVFDILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLK 180
 |||
 Db 98 RYSVFDILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLK 157

Qy 181 MVGGWPVAMDKWNETMGLKWELERQLAVLNSQFNRRVLIDLFIWNDDQNSSRHVIYIDQP 240
 ||||| : |||||
 Db 158 MVGGWPVALDKWNETMGLKWELERQLAVLNSQFNRRVLIDLFIWNDDQNSSRHVIYIDQP 217
 Qy 241 TLGMPsREYYFQEDNNHKVRKAYLEFMTSVATMLRKDQNLskESAMVREEMAeVLELETh 300
 ||||| |||||
 Db 218 TLGMPsREYYFQEDNNHKVRKAYPEFMTSVATMLRKDQNLskESAMVREEMAeVLELETh 277
 Qy 301 LANATVPQEKRHdVTALYHRMDLMELQERFGLKGFNWTLFIQNLSSVEVELFPDEEVV 360
 ||||| |||||
 Db 278 LANATVPQEKRHdVTALYHRMDLMELQERFGLKGFNWTLFIQNLSSVEVELFPDEEVV 337
 Qy 361 YGIPYLENLEDIIDSYSARTMQNYLVRLVLDRIgSLsQRfKEARVDYRKALYgTTVEEV 420
 ||||| |||||
 Db 338 YGIPYLENLEDIIDSYSARTMQNYLVRLVLDRIgSLsQRfKEARVDYRKALYgTTVEEV 397
 Qy 421 RWRECVSYVNSNMESAVGSLYIKRAFskDSKSTVRELIEKIRSVFVDNLDELNWMDEESK 480
 ||||| |||||
 Db 398 RWRECVSYVNSNMESAVGSLYIKRAFskDSKSTVRELIEKIRSVFVDNLDELNWMDEESK 457
 Qy 481 KKAQEKAMNIREQIGYPDYILEDNNKHLDEEYSSLTFYEDLYFENGLQNLKNNaQRSLKk 540
 ||||| |||||
 Db 458 KKAQEKAMNIREQIGYPDYILEDNNKHLDEEYSSLTFYEDLYFENGLQNLKNNaQRSLKk 517
 Qy 541 LREKVDQNLWIIGAaVVNAFYSPNRNQIVFPAGILQPPFFSKDQPQSLNFGGIGMvIGHE 600
 ||||| |||||
 Db 518 LREKVDQNLWIIGAaVVNAFYSPNRNQIVFPAGILQPPFFSKDQPQSLNFGGIGMvIGHE 577
 Qy 601 ITHGFDDNGRNFDKNGNMLDWWSNFSARHFQQSQCMiYQYGNFSWELADNQNVNGFSTL 660
 ||||| ||||| : |
 Db 578 ITHGFDDNGRNFDKNGNMLDWWSNFSARHFQQSQCMiYQYGNFSWELADNQNVNGFSSL 637
 Qy 661 GENIADNGGVRQAYKAYLRWLADGGKDQRLPGLNLTyaQLFFINyaQVWCGSYRPEFAVQ 720
 ||||| |||||
 Db 638 GENIADNGGVRQAYKAYLRWLADGGKDQRLPGLNLTyaQLFFINyaQVWCGSYRPEFAVQ 697
 Qy 721 SIKTDVHSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPMKRCRIW 765
 ||||| |||||
 Db 698 SIKTDVHSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPMKRCRIW 742

RESULT 5

Q9ERK2

ID Q9ERK2 PRELIMINARY; PRT; 779 AA.
 AC Q9ERK2;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Neprilysin-like peptidase gamma.
 GN MELL1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21293028; PubMed=11278416;
 RA Shirovani K., Tsubuki S., Iwata N., Takaki Y., Harigaya W.,
 RA Maruyama K., Kiryu-Seo S., Kiyama H., Iwata H., Tomita T.,
 RA Iwatsubo T., Saido T.C.;
 RT "Neprilysin Degrades Both Amyloid beta Peptides 1-40 and 1-42 Most
 RT Rapidly and Efficiently among Thiorphan- and Phosphoramidon-sensitive
 RT Endopeptidases."
 RL J. Biol. Chem. 276:21895-21901(2001).
 DR EMBL; AF302077; AAG18448.1; -.
 DR HSSP; P08473; 1DMT.
 DR MEROPS; M13.008; -.
 DR MGD; MGI:1351603; Mell1.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0005794; C:Golgi apparatus; IDA.
 DR InterPro; IPR000718; Peptidase_M13.
 DR InterPro; IPR008753; Peptidase_M13_N.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR Pfam; PF01431; Peptidase_M13; 1.
 DR Pfam; PF05649; Peptidase_M13_N; 1.
 DR PRINTS; PR00786; NEPRILYSIN.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 SQ SEQUENCE 779 AA; 89709 MW; 5E48CA530828584B CRC64;

Query Match 95.8%; Score 3872; DB 11; Length 779;
 Best Local Similarity 92.5%; Pred. No. 5.5e-227;
 Matches 742; Conservative 0; Mismatches 0; Indels 60; Gaps 2;

Qy	1	MVERAGWCRKKS	PGFVEYGLMVLLLLLL	LGAI	VT	LG	VF	YS	IG	KQ	LP	LL	TS	LL	HF	SW	DERTV	60
Db	1	MVERAGWCRKKS	PGFVEYGLMVLLLLLL	LGAI	VT	LG	VF	YS	I	-----	-----	-----	-----	-----	-----	-----	-----	40
Qy	61	VKRALR	DSSLKSDICT	TPSCVIAAAR	I	LENMDQSR	NP	CENFYQYAC	GGWLR	RHHV	IP	ETNS	120					
Db	41	---	ALRDSSLKSDICT	TPSCVIAAAR	I	LENMDQSR	NP	CENFYQYAC	GGWLR	RHHV	IP	ETNS	97					
Qy	121	RYSVFDILR	DELEVILKGV	LEDSTS	QHRPAVEK	AKTLYR	SCMNQSV	IEKRDSE	PLLSV	LK	180							
Db	98	RYSVFDILR	DELEVILKGV	LEDSTS	QHRPAVEK	AKTLYR	SCMNQSV	IEKRDSE	PLLSV	LK	157							
Qy	181	MVGGWPV	AMDKWNETM	GLKWELER	QLAVLNSQ	FNRRVLI	DLFIW	NDDQNS	SRHVI	YIDQP	240							
Db	158	MVGGWPV	AMDKWNETM	GLKWELER	QLAVLNSQ	FNRRVLI	DLFIW	NDDQNS	SRHVI	YIDQP	217							

Qy 241 TLGMPREYYFQEDNNHKVRKAYLEFMTSVATMLRKDQNLKESAMVREEMAQVLELETH 300
 |||||
 Db 218 TLGMPREYYFQEDNNHKVRKAYLEFMTSVATMLRKDQNLKESAMVREEMAQVLELETH 277
 Qy 301 LANATVPQEKRDVTALYHRMDLMELQERF----- 330
 |||||
 Db 278 LANATVPQEKRDVTALYHRMDLMELQERFGLKDRVSLCSPGCPGTHSVDQAGLELGNPP 337
 Qy 331 -----GLKGFNWTLFIQNVLSSVEVELFPDEEVVYVYGIPLYENLEDIIDSYSARTMQN 383
 |||||
 Db 338 ASDSRVLGLKGFNWTLFIQNVLSSVEVELFPDEEVVYVYGIPLYENLEDIIDSYSARTMQN 397
 Qy 384 YLVWRLVLDRIQSLQRFKEARVDYRKALYGTTVVEEVRWRECVSYVNSNMESAVGSLYIK 443
 |||||
 Db 398 YLVWRLVLDRIQSLQRFKEARVDYRKALYGTTVVEEVRWRECVSYVNSNMESAVGSLYIK 457
 Qy 444 RAFSKDSKSTVRELIEKIRSVFVDNLDELNWMDEESKKKAQEKAMNIREQIGYDPDYILED 503
 |||||
 Db 458 RAFSKDSKSTVRELIEKIRSVFVDNLDELNWMDEESKKKAQEKAMNIREQIGYDPDYILED 517
 Qy 504 NNLHLDEEYSSLTFYEDLYFENGLQNLKNNARSLKLRKVDQNLWIIGAAVVNAFYSP 563
 |||||
 Db 518 NNLHLDEEYSSLTFYEDLYFENGLQNLKNNARSLKLRKVDQNLWIIGAAVVNAFYSP 577
 Qy 564 NRNQIVFPAGILQPPFFSKDQPQSLNFGGIGMVGHEITHGFDDNGRNFDKNGNMLDWW 623
 |||||
 Db 578 NRNQIVFPAGILQPPFFSKDQPQSLNFGGIGMVGHEITHGFDDNGRNFDKNGNMLDWW 637
 Qy 624 NFSARHFQQSQCMYQYGNFSWELADNQNNGFSTLGENIADNGGVRQAYKAYLRWLAD 683
 |||||
 Db 638 NFSARHFQQSQCMYQYGNFSWELADNQNNGFSTLGENIADNGGVRQAYKAYLRWLAD 697
 Qy 684 GGDQRLPGLNLTAYQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQNLPG 743
 |||||
 Db 698 GGDQRLPGLNLTAYQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQNLPG 757
 Qy 744 FSEAFHCPRGSPMHPMKRCRIW 765
 |||||
 Db 758 FSEAFHCPRGSPMHPMKRCRIW 779